

O I P E
JUN 16 2005
P A T E N T & T R A D E M A R K O F F I C E

OBLON ET AL (703) 413-3000
DOCKET # 213993US0PCT
INV. MARECHAL, Eric, et. al.
USSN 09/926,169
Reply to N.R.D. DATED April 29, 2005
REPLACEMENT DRAWINGS

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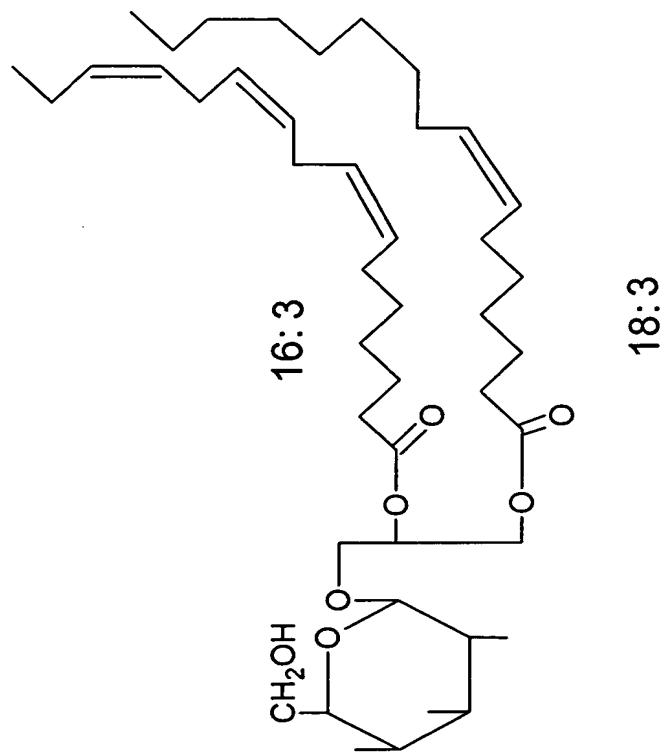


FIG. 1



soMGD A MSHPSTVTSEPSN-LLDFVPKLGPNFVLNSSLHGNNNSGYSFSSNSVHFGGLAT---QN 55
 csMGD A MRNPSTVQENG-VSDFISQLGYFAFSSRFLNLNSEGCSSSSHSLYLNGFENYRCVKR 59
 atMGD A MQNPSTVTQESAAPVFDFFPRLRGLTSRNRSPCSNSDGYALSSSNALYFNGFRTLPS-RR 59
 atMGD B -----

soMGD A RYKFNNSLSF---SKEGSNLKRILSDFNRVIRLHCDRI-PLGFSSIGLN--SGESNGVSD 109
 csMGD A PPRSGASLSLS---SRGSSSLRRFVNEFNNVIKFHCHKP-PLGFASLGGV--SDETNGIRD 114
 atMGD A MGKTLASLSFNTKSSAGSSLRRFISDFNSFIRFHCDKVVPEFASVGGVGLSSDENGIRE 119
 atMGD B ---MATTVM---ALAEKVLERYVGTSKSAVSVTSGDGEKTHRHTHHHIHRRIKSYDDIDE 53
 : : : : *::: : : : : : : : : | : : :::: :
 soMGD A NGHG-VLEDVRVPVNAVEPESPKRVLILMSDTGGGHRASAEAIAKAFFNEEFGDDYQVFVT 168
 csMGD A DFGF-VSODGALPLNKIEAENPKRVLILMSDTGGGHRASAEAIAKAFFNEEFGNNYQVFIT 173
 atMGD A NGTGGVLGEEGGLPLNGVEADRPKKVLILMSDTGGGHRASAEAIARAAFNQEFGDEYQVFIT 179
 atMGD B DESS-----LELIQIGAERTKVNVLILMSDTGGGHRASAEAIAIRDAFKIEFGDKYRVIVK 106
 : : : : : : : *:*****:*****: *: *: *: *: :
 h1

soMGD A DLWSEHTPWPFNQLPRSYNFLVKHGPLWKMMYYGTSPRVIHQSNFAATSVFIAREVARGL 228
 csMGD A DLWTDHTPWPFNQLPRSYNFLVKHGTWLKMTYYTAPKVIHQSNFAATSTFIAREVAKGL 233
 atMGD A DLWTDHTPWPFNQLPRSYNFLVKHGTWLKMTYYGTSPRIVHQSNFAATSTFIAREIAQGL 239
 atMGD B DVWKEYTGWPLNDMERSYKFMVKHVQLWKVAFHSTSPKWIHSCYLAIAAYAKEVAGL 166
 *:
 h2*

soMGD A MKYQDPDIIISVHPLMQHVPLRILRGRGLLEKIVFTTVTDLSTCHPTWFHKLVTRCYCPS 288
 csMGD A MKYRPDIIISVHPLMQHVPIRILRSKGLLNKIVFTTVTDLSTCHPTWFHKLVTRCYCPS 293
 atMGD A MKYQDPDIIISVHPLMQHVPLRVLRLRSKGLKKIVFTTVTDLSTCHPTWFHKLVTRCYCPS 299
 atMGD B MEYKPEIIISVHPLMQHIPLWVLWKQELQKRVLFVTVIDLNTCHPTWFHPGVNRCYCPS 226
 *: *: *: *: *: *: *: *: *: *: *: *: *: *: *: *: *: *: *:
 h3*

soMGD A NEVAKRATKAGLQPSQIKVYGLPVRFPSVRSVPKNELRKELGMDEHLPAVLLMGGEGM 348
 csMGD A TEVAKRALTAGLQPSKLKVFGLPVRFPSFKPIRPKIELRKELGMDENLPAVLLMGGEGM 353
 atMGD A TEVAKRAQKAGLETSQIKVYGLPVRFPSFKPVRPKVELRRELGMDENLPAVLLMGGEGM 359
 atMGD B QEVAKRALFDGLDESQVRVFGLPVRFPSFARAVLVKDDLRKELEMDQDLRAVLLMGGEGM 286
 *: *: *: *: *: *: *: *: *: *: *: *: *: *: *: *: *: *:
 h4

soMGD A GPIEATARALGNALYDANLGEPTGQLLVICGRNKKLAGKLSSIDWKIPVQVKGFVTKIEE 408
 csMGD A GPIEATAKALSKALYDENHGEPIGQVLVICGHNNKKLAGRLRSIDWKVPPVQVKGFVTKME 413
 atMGD A GPIEATARALADALYDKNLGEAVGQVLIICGRNKKLQSKLSSLDWKIPVQVKGFITKME 419
 atMGD B GPVKETAKALEEFLYDKENRKPIGQMVVICGRNKKLASALEAIDWKIPVVKVRGFETQMEK 346
 *: *: *: *: *: *: *: *: *: *: *: *: *: *: *: *: *:
 h5*

soMGD A CMGACDCIITKAGPGTIAEAMIRGLPPILNDDYIAGQEAQNVYVIENGIGKYLKSPKEIA 468
 csMGD A CMGACDCIITKAGPGTIAEAMIRGLPPILNDDYIAGQEAQNVYVVENGCCKFSKSPKEIA 473
 atMGD A CMGACDCIITKAGPGTIAEAMIRGLPPILNDDYIAGQEAQNVYVVENGCCKFSKSPKEIS 479
 atMGD B WMGACDCIITKAGPGTIAESLIRSLPPILNDDYIAGQEAQNVYVVENGAGVFTRSPKETA 406
 *: *: *: *: *: *: *: *: *: *: *: *: *:
 h6*

soMGD A KTVSQWFGPKANELQIMSQNALKHARPDVKIVHDLDELVRQKIFVQRQYSCAA----- 522
 csMGD A NIVAKWFGPKADELLIMSQNALRLARPDAVKIVHDLHFLVKQRSFVPPQYSG----- 525
 atMGD A KIVADWFGPASKELEIMSQNALRLAKPEAVFKIVHDMHELVKKNSLPQLSCTA----- 533
 atMGD B RIVGEWFSTKTDELEQTSDNARKLAQPEAVFDIVKIDELSEQRGPLASVSYNLTSFASLV 468
 *: *: *: *: *: *: *: *: *: *: *: *: *:
 h7*

FIG. 2A

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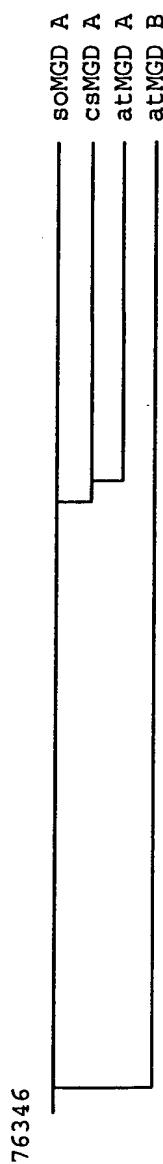


FIG. 2B

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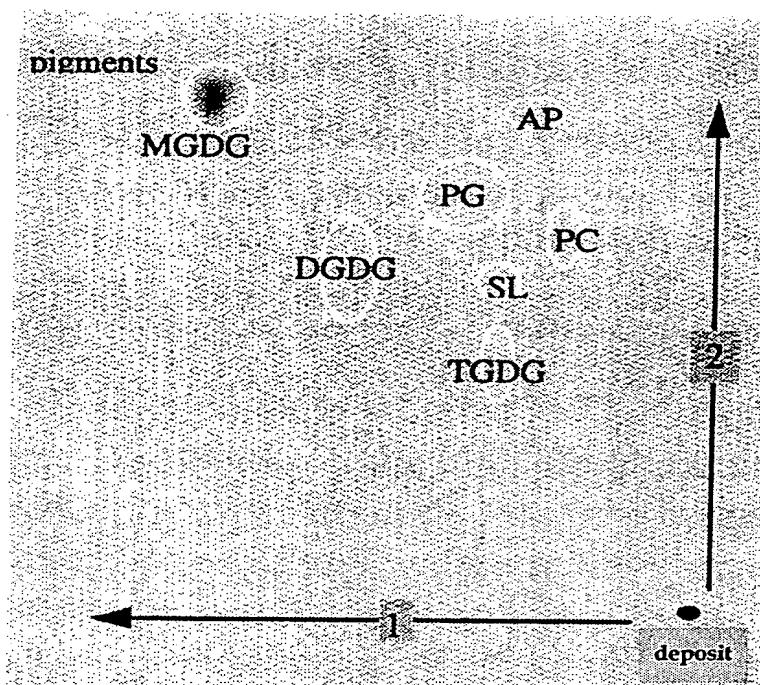


FIG. 3A

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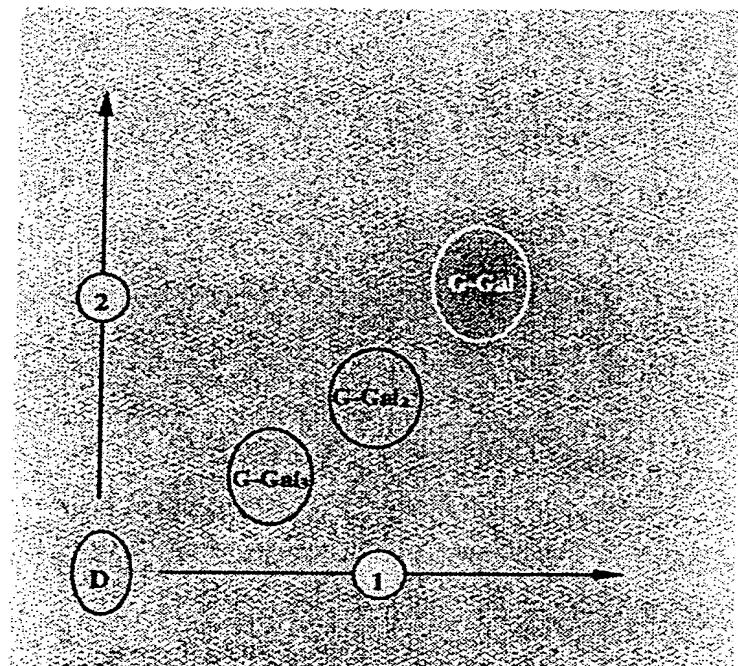


FIG. 3B

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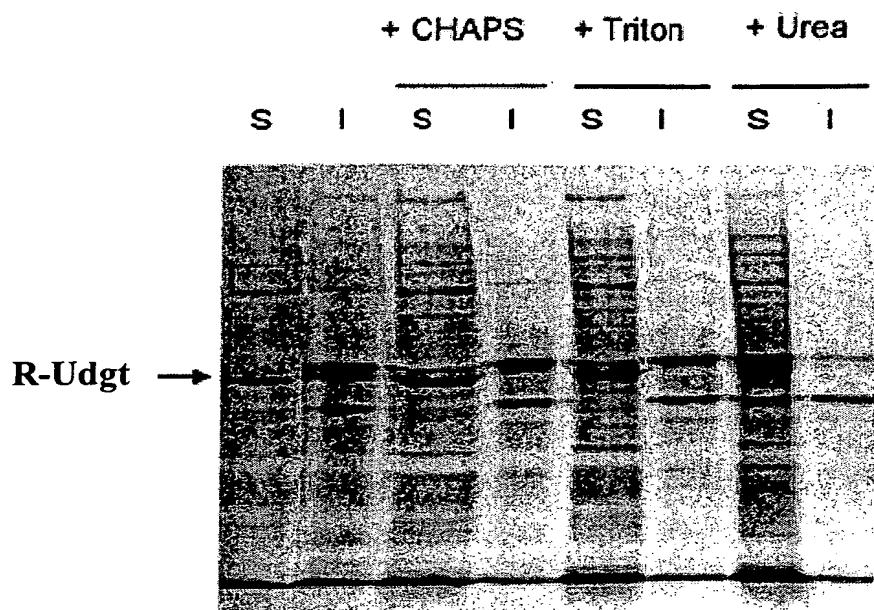


FIG. 4

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FIG. 5A

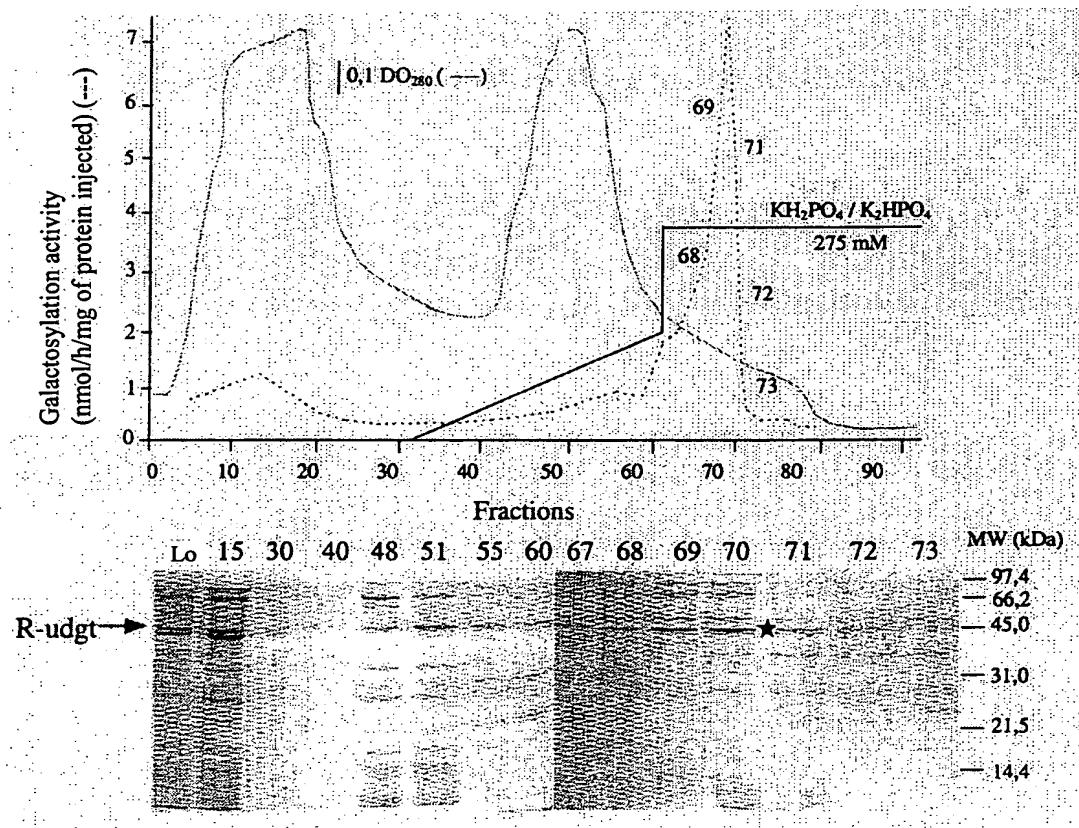


FIG. 5B